

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/846,658B

1642

Page # 12

DATE: 08/18/98
TIME: 09:57:42

INPUT SET: S28075.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Adair, John R.
6 Athwal, Diljeet S.
7 Emtage, John S.
8
9 (ii) TITLE OF INVENTION: Humanised Antibodies
10
11 (iii) NUMBER OF SEQUENCES: 30
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
15 (B) STREET: One Liberty Place - 46th Floor
16 (C) CITY: Philadelphia
17 (D) STATE: PA
18 (E) COUNTRY: USA
19 (F) ZIP: 19103
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: US 08/846,658
29 (B) FILING DATE: 01-MAY-1997
30 (C) CLASSIFICATION:
31
32 (viii) ATTORNEY/AGENT INFORMATION:
33 (A) NAME: Trujillo, Doreen Yatko
34 (B) REGISTRATION NUMBER: 35,719
35 (C) REFERENCE/DOCKET NUMBER: CARP-0057
36
37 (ix) TELECOMMUNICATION INFORMATION:
38 (A) TELEPHONE: (215) 568-3100
39 (B) TELEFAX: (215) 568-3439
40
41
42 (2) INFORMATION FOR SEQ ID NO:1:
43
44 (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 20 base pairs
46 (B) TYPE: nucleic acid

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47 (C) STRANDEDNESS: single
48 (D) TOPOLOGY: linear
49
50 (ii) MOLECULE TYPE: cDNA
51
52
53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
54
55 TCCAGATGTT AACTGCTCAC 20
56
57 (2) INFORMATION FOR SEQ ID NO:2:
58
59 (i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 23 base pairs
61 (B) TYPE: nucleic acid
62 (C) STRANDEDNESS: single
63 (D) TOPOLOGY: linear
64
65 (ii) MOLECULE TYPE: cDNA
66
67
68
69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
70
71 CAGGGGCCAG TGGATGGATA GAC 23
72
73 (2) INFORMATION FOR SEQ ID NO:3:
74
75 (i) SEQUENCE CHARACTERISTICS:
76 (A) LENGTH: 9 amino acids
77 (B) TYPE: amino acid
78 (C) STRANDEDNESS: single
79 (D) TOPOLOGY: linear
80
81 (ii) MOLECULE TYPE: peptide
82
83
84
85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
86
87 Leu Glu Ile Asn Arg Thr Val Ala Ala
88 1 5
89
90 (2) INFORMATION FOR SEQ ID NO:4:
91
92 (i) SEQUENCE CHARACTERISTICS:
93 (A) LENGTH: 943 base pairs
94 (B) TYPE: nucleic acid
95 (C) STRANDEDNESS: single
96 (D) TOPOLOGY: linear
97
98 (ii) MOLECULE TYPE: cDNA
99

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100
101      (ix) FEATURE:
102          (A) NAME/KEY: CDS
103          (B) LOCATION: 18..722
104
105      (ix) FEATURE:
106          (A) NAME/KEY: mat_peptide
107          (B) LOCATION: 84..722
108
109
110      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
111
112      GAATTCCTCAA AGACAAA ATG GAT TTT CAA GTG CAG ATT TTC AGC TTC CTG      50
113          Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu
114          -22      -20      -15
115
116      CTA ATC AGT GCC TCA GTC ATA ATA TCC AGA GGA CAA ATT GTT CTC ACC      98
117      Leu Ile Ser Ala Ser Val Ile Ile Ser Arg Gly Gln Ile Val Leu Thr
118          -10      -5      1      5
119
120      CAG TCT CCA GCA ATC ATG TCT GCA TCT CCA GGG GAG AAG GTC ACC ATG      146
121      Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met
122          10      15      20
123
124      ACC TGC AGT GCC AGC TCA AGT GTA AGT TAC ATG AAC TGG TAC CAG CAG      194
125      Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
126          25      30      35
127
128      AAG TCA GGC ACC TCC CCC AAA AGA TGG ATT TAT GAC ACA TCC AAA CTG      242
129      Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu
130          40      45      50
131
132      GCT TCT GGA GTC CCT GCT CAC TTC AGG GGC AGT GGG TCT GGG ACC TCT      290
133      Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser
134          55      60      65
135
136      TAC TCT CTC ACA ATC AGC GGC ATG GAG GCT GAA GAT GCT GCC ACT TAT      338
137      Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr
138          70      75      80      85
139
140      TAC TGC CAG CAG TGG AGT AGT AAC CCA TTC ACG TTC GGC TCG GGG ACA      386
141      Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr
142          90      95      100
143
144      AAG TTG GAA ATA AAC CGG GCT GAT ACT GCA CCA ACT GTA TCC ATC TTC      434
145      Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Val Ser Ile Phe
146          105      110      115
147
148      CCA CCA TCC AGT GAG CAG TTA ACA TCT GGA GGT GCC TCA GTC GTG TGC      482
149      Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys
150          120      125      130
151
152      TTC TTG AAC AAC TTC TAC CCC AAA GAC ATC AAT GTC AAG TGG AAG ATT      530

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153 Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile
154      135                      140                      145
155
156
157 GAT GGC AGT GAA CGA CAA AAT GGC GTC CTG AAC AGT TGG ACT GAT CAG      578
158 Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln
159 150                      155                      160                      165
160
161 GAC AGC AAA GAC AGC ACC TAC AGC ATG AGC AGC ACC CTC ACG TTG ACC      626
162 Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr
163                      170                      175                      180
164
165 AAG GAC GAG TAT GAA CGA CAT AAC AGC TAT ACC TGT GAG GCC ACT CAC      674
166 Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His
167      185                      190                      195
168
169 AAG ACA TCA ACT TCA CCC ATT GTC AAG AGC TTC AAC AGG AAT GAG TGT      722
170 Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
171      200                      205                      210
172
173 TAGAGACAAA GGTCCGTGAGA CGCCACCACC AGCTCCCAGC TCCATCCCTAT CTTCCCTTCT      782
174
175 AAGGTCTTGG AGGCTTCCCC ACAAGCGCTT ACCACTGTGTG CGGTGCTCTA AACCTCCTCC      842
176
177 CACCTCCTTC TCCTCCTCCT CCCTTTCCTT GGCTTTTATC ATGCTAATAT TTGCAGAAAA      902
178
179 TATTCAATAA AGTGAGTCTT TGCCTTGAAA AAAAAAAAAA A      943
180
181
182 (2) INFORMATION FOR SEQ ID NO:5:
183
184 (i) SEQUENCE CHARACTERISTICS:
185 (A) LENGTH: 235 amino acids
186 (B) TYPE: amino acid
187 (D) TOPOLOGY: linear
188
189 (ii) MOLECULE TYPE: protein
190
191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
192
193 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
194 -22      -20                      -15                      -10
195
196 Val Ile Ile Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
197      -5                      1                      5                      10
198
199 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
200                      15                      20                      25
201
202 Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser
203      30                      35                      40
204
205 Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro

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	45	50	55
206			
207			
208	Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile		
209	60	65	70
210			
211	Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp		
212	75	80	85
213			90
214			
215	Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn		
216		95	100
217			105
218	Arg Ala Asp Thr Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu		
219		110	115
220			120
221	Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe		
222		125	130
223			135
224	Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg		
225		140	145
226			150
227	Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser		
228		155	160
229			165
230	Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu		
231		175	180
232			185
233	Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser		
234		190	195
235			200
236	Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys		
237		205	210
238			

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 41..1444

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 98..1444

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SEQUENCE VERIFICATION REPORT
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Original Text